

RAW SEQUENCE LISTING

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Application Serial Number: 10/825,026

Source: IFW

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IFWO

RAW SEQUENCE LISTING

DATE: 01/13/2005

PATENT APPLICATION: US/10/825,026

TIME: 11:37:16

Input Set : D:\03-03-US.ST25.txt

Output Set: N:\CRF4\01132005\J825026.raw

3 <110> APPLICANT: Aventis Pasteur, Ltd.
 5 <120> TITLE OF INVENTION: Tumor Antigen BFA-5 for Prevention and/or Treatment of
 Cancer

7 <130> FILE REFERENCE: API-03-03-US
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/825,026

C--> 9 <141> CURRENT FILING DATE: 2004-04-15

9 <150> PRIOR APPLICATION NUMBER: 60/462,945

10 <151> PRIOR FILING DATE: 2004-04-15

12 <160> NUMBER OF SEQ ID NOS: 106

14 <170> SOFTWARE: PatentIn version 3.2

16 <210> SEQ ID NO: 1

17 <211> LENGTH: 3846

18 <212> TYPE: DNA

19 <213> ORGANISM: Homo sapiens

21 <400> SEQUENCE: 1

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24	ctggagccta	taggtacaga	aagcaaggta	tctggaaaga	acaaagaatt	ctctgcagat	120
26	cagatgtcag	aaaatacgga	tcagagtgat	gctgcagaac	taaatcataa	ggaggaacat	180
28	agcttgcatg	ttcaagatcc	atcttctagc	agtaagaagg	acttgaaaag	cgcagttctg	240
30	agtgagaagg	ctggcttcaa	ttatgaaagc	cccagtaagg	gaggaaaact	tccctccttt	300
32	ccgcattgat	aggtgacaga	cagaaatatg	ttggctttct	catttccagc	tgctggggga	360
34	gtctgtgagc	ccttgaagtc	tccgcaaaga	gcagaaggcag	atgaccctca	agatatggcc	420
36	tgcacccctc	caggggactc	actggagaca	aaggaagatc	agaagatgtc	accaaaggct	480
38	acagaggaaa	cagggcaagc	acagagtggg	caagccaatt	gtcaagggtt	gagcccagtt	540
40	tcagtggcct	caaaaaaccc	acaagtgcct	tcagatgggg	gtgtaagact	gaataaatcc	600
42	aaaactgact	tactgggtgaa	tgacaaccca	gaccgggcac	ctctgtctcc	agagcttcag	660
44	gacttttaaat	gcaatatctg	tggatatggg	tactacggca	acgacccac	agatctgatt	720
46	aagcacttcc	gaaagtatca	cttaggactg	cataaccgca	ccaggcaaga	tgctgagctg	780
48	gacagcaaaa	tcttggccct	tcataacatg	gtgcagttca	gccattccaa	agacttccag	840
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54	cggaaaacac	cagattgccca	agggaaacac	aagtatttcc	gctgtaaatt	ctgcaatttc	1020
56	acttatatgg	gcaactcatc	caccgaatta	gaacaacatt	ttcttcagac	tcacccaaac	1080
58	aaaataaaaag	cttctctctcc	ctcctctgag	gttgcaaaaac	cttcagagaa	aaactctaac	1140
60	aagtccatcc	ctgcacttca	atccagtgat	tctggagact	tgggaaaatg	gcaggacaag	1200
62	ataacagtca	aagcaggaga	tgacactcct	gttgggtact	cagtgcccat	aaagcccctc	1260
64	gattcctcta	gacaaaatgg	tacagaggcc	accagttact	actggtgtaa	atcttgtagt	1320
66	ttcagctgtg	agtcattctag	ctcacttaaa	ctgctagaac	attatggcaa	gcagcacgga	1380
68	gcagtgcagt	caggcggcct	taatccagag	ttaaatgata	agctttccag	gggctctgtc	1440
70	attaatcaga	atgatctagc	caaaagtcca	gaaggagaga	caatgaccaa	gacagacaag	1500
72	agctcgagtg	gggctaaaaa	gaaggacttc	tccagcaagg	gagccgagga	taatattgga	1560
74	acgagctata	attgtcagtt	ctgtgacttc	cgatattcca	aaagccatgg	ccctgatgta	1620
76	attgtagtgg	ggccacttct	ccgtcattat	caacagctcc	ataacattca	caagtgtacc	1680
78	attaaacact	gtccattctg	tcccagagga	ctttgcagcc	cagaaaagca	ccttgagaaa	1740

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80 attacttattc cgtttgcttg tagaaaaagt aattgttccc actgtgcact cttgcttctg 1800
82 cacttgctctc ctggggcggc tgaagctcg cgagtcaaac atcagtgcc tcaagtgttca 1860
84 ttcaccaccc ctgacgtaga tgtactcctc tttcactatg aaagtgtgca tgagtcccaa 1920
86 gcatcgcatg tcaaacaaga agcaaatcac ctgcaaggat cggatgggca gcagtctgtc 1980
88 aaggaaaagca aagaacactc atgtaccaa tgtgatttta ttacccaagt ggaagaagag 2040
90 atttcccagc actacaggag agcacacagc tgctacaaat gccgtcagt cagttttaca 2100
92 gctgccgata ctgagtcact actggagcac ttcaacactg ttcactgcc ggaacaggac 2160
94 atcactacag ccaacggcga agaggacggg catgccatat ccaccatcaa agaggagccc 2220
96 aaaattgact tcagggtcta caatctgcta actccagact ctaaaatggg agagccagtt 2280
98 tctgagagtg tgggtgaagag agagaagctg gaagagaagg acgggctcaa agagaaagtt 2340
100 tggaccgaga gttccagtga tgaccttcgc aatgtgactt ggagaggggc agacatcctg 2400
102 cgggggagtc cgtcatcac ccaagcaagc ctggggctgc tgacgcctgt gtctggcacc 2460
104 caagagcaga caaagactct aagggatagt cccaatgtgg aggccgcca tctggcgca 2520
106 cctatttatg gcttggctgt ggaaaccaag ggattcctgc agggggcgcc agctggcgga 2580
108 gagaagtctg gggccctccc ccagcagtat cctgcatcg gagaaaacaa gtccaaggat 2640
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112 accacaaaga cctctctctg gcgaaagaat gcaaatggcg gatatgtat caacgcgtgt 2760
114 ggcctctacc agaagcttca ctgactccc aggcctttaa acatcattaa acaaaacaac 2820
116 ggtgagcaga ttattaggag gagaacaaga aagcgcctta acccagaggc acttcaggct 2880
118 gagcagctca acaaacagca gaggggcagc aatgaggagc aagtcaatgg aagcccgtta 2940
120 gagaggaggt cagaagatca tctaactgaa agtcaccaga gagaaattcc actccccagc 3000
122 ctaagtaaat acgaagccca gggttcattg actaaaagcc attctgctca gcagccagtc 3060
124 ctggtcagcc aaactctgga tattcacaaa aggatgcaac ctttgcacat tcagataaaa 3120
126 agtcctcagg aaagtactgg agatccagga aatagttcat ccgtatctga agggaaagga 3180
128 agttctgaga gaggcagtcc tatagaaaag tacatgagac ctgcgaaaca cccaaattat 3240
130 tcaccaccag gcagccctat tgaaaagtac cagtaccac tttttggact tccctttgta 3300
132 cataatgact tccagagtga agctgattgg ctgcggttct ggagtaaata taagctctcc 3360
134 gttcctggga attccgacta cttgactcac gtgacctggc taccaaatcc ttgccaaaac 3420
136 tatgtgcctt atcccacctt caatctgcct cctcattttt cagctgttgg atcagacaat 3480
138 gacattcctc tagatttggc gatcaagcat tccagacctg ggccaactgc aaacggtgcc 3540
140 tccaaggaga aaacgaaggc accaccaaat gtaaaaaatg aaggtccctt gaatgtagta 3600
142 aaaacagaga aagttgatag aagtactcaa gatgaacttt caacaaaatg tgtgcactgt 3660
144 ggcattgtct ttctggatga agtgatgtat gctttgcata tgagttgcca tgggtgacagt 3720
146 ggacctttcc agtgcagcat atgccagcat ctttgcacgg acaaatatga cttcacaaca 3780
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153 <210> SEQ ID NO: 2

154 <211> LENGTH: 1281

155 <212> TYPE: PRT

156 <213> ORGANISM: Homo sapiens

158 <400> SEQUENCE: 2

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161 1 5 10 15
164 Glu Gly Gln Ile Leu Glu Pro Ile Gly Thr Glu Ser Lys Val Ser Gly
165 20 25 30
168 Lys Asn Lys Glu Phe Ser Ala Asp Gln Met Ser Glu Asn Thr Asp Gln
169 35 40 45
172 Ser Asp Ala Ala Glu Leu Asn His Lys Glu Glu His Ser Leu His Val
173 50 55 60

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176 Gln Asp Pro Ser Ser Ser Ser Lys Lys Asp Leu Lys Ser Ala Val Leu
177 65              70              75              80
180 Ser Glu Lys Ala Gly Phe Asn Tyr Glu Ser Pro Ser Lys Gly Gly Asn
181              85              90              95
184 Phe Pro Ser Phe Pro His Asp Glu Val Thr Asp Arg Asn Met Leu Ala
185              100             105             110
188 Phe Ser Phe Pro Ala Ala Gly Gly Val Cys Glu Pro Leu Lys Ser Pro
189              115             120             125
192 Gln Arg Ala Glu Ala Asp Asp Pro Gln Asp Met Ala Cys Thr Pro Ser
193              130             135             140
196 Gly Asp Ser Leu Glu Thr Lys Glu Asp Gln Lys Met Ser Pro Lys Ala
197 145              150             155             160
200 Thr Glu Glu Thr Gly Gln Ala Gln Ser Gly Gln Ala Asn Cys Gln Gly
201              165              170             175
204 Leu Ser Pro Val Ser Val Ala Ser Lys Asn Pro Gln Val Pro Ser Asp
205              180             185             190
208 Gly Gly Val Arg Leu Asn Lys Ser Lys Thr Asp Leu Leu Val Asn Asp
209              195             200             205
212 Asn Pro Asp Pro Ala Pro Leu Ser Pro Glu Leu Gln Asp Phe Lys Cys
213              210             215             220
216 Asn Ile Cys Gly Tyr Gly Tyr Tyr Gly Asn Asp Pro Thr Asp Leu Ile
217 225              230             235             240
220 Lys His Phe Arg Lys Tyr His Leu Gly Leu His Asn Arg Thr Arg Gln
221              245             250             255
224 Asp Ala Glu Leu Asp Ser Lys Ile Leu Ala Leu His Asn Met Val Gln
225              260             265             270
228 Phe Ser His Ser Lys Asp Phe Gln Lys Val Asn Arg Ser Val Phe Ser
229              275             280             285
232 Gly Val Leu Gln Asp Ile Asn Ser Ser Arg Pro Val Leu Leu Asn Gly
233              290             295             300
236 Thr Tyr Asp Val Gln Val Thr Ser Gly Gly Thr Phe Ile Gly Ile Gly
237 305              310             315             320
240 Arg Lys Thr Pro Asp Cys Gln Gly Asn Thr Lys Tyr Phe Arg Cys Lys
241              325             330             335
244 Phe Cys Asn Phe Thr Tyr Met Gly Asn Ser Ser Thr Glu Leu Glu Gln
245              340             345             350
248 His Phe Leu Gln Thr His Pro Asn Lys Ile Lys Ala Ser Leu Pro Ser
249              355             360             365
252 Ser Glu Val Ala Lys Pro Ser Glu Lys Asn Ser Asn Lys Ser Ile Pro
253              370             375             380
256 Ala Leu Gln Ser Ser Asp Ser Gly Asp Leu Gly Lys Trp Gln Asp Lys
257 385              390             395             400
260 Ile Thr Val Lys Ala Gly Asp Asp Thr Pro Val Gly Tyr Ser Val Pro
261              405             410             415
264 Ile Lys Pro Leu Asp Ser Ser Arg Gln Asn Gly Thr Glu Ala Thr Ser
265              420             425             430
268 Tyr Tyr Trp Cys Lys Phe Cys Ser Phe Ser Cys Glu Ser Ser Ser Ser
269              435             440             445
272 Leu Lys Leu Leu Glu His Tyr Gly Lys Gln His Gly Ala Val Gln Ser

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273	450					455					460							
276	Gly	Gly	Leu	Asn	Pro	Glu	Leu	Asn	Asp	Lys	Leu	Ser	Arg	Gly	Ser	Val		
277	465						470						475	480				
280	Ile	Asn	Gln	Asn	Asp	Leu	Ala	Lys	Ser	Ser	Glu	Gly	Glu	Thr	Met	Thr		
281						485						490	495					
284	Lys	Thr	Asp	Lys	Ser	Ser	Ser	Gly	Ala	Lys	Lys	Lys	Asp	Phe	Ser	Ser		
285						500						505	510					
288	Lys	Gly	Ala	Glu	Asp	Asn	Met	Val	Thr	Ser	Tyr	Asn	Cys	Gln	Phe	Cys		
289						515						520	525					
292	Asp	Phe	Arg	Tyr	Ser	Lys	Ser	His	Gly	Pro	Asp	Val	Ile	Val	Val	Gly		
293						530						535	540					
296	Pro	Leu	Leu	Arg	His	Tyr	Gln	Gln	Leu	His	Asn	Ile	His	Lys	Cys	Thr		
297	545						550						555	560				
300	Ile	Lys	His	Cys	Pro	Phe	Cys	Pro	Arg	Gly	Leu	Cys	Ser	Pro	Glu	Lys		
301						565						570	575					
304	His	Leu	Gly	Glu	Ile	Thr	Tyr	Pro	Phe	Ala	Cys	Arg	Lys	Ser	Asn	Cys		
305						580						585	590					
308	Ser	His	Cys	Ala	Leu	Leu	Leu	Leu	His	Leu	Ser	Pro	Gly	Ala	Ala	Gly		
309						595						600	605					
312	Ser	Ser	Arg	Val	Lys	His	Gln	Cys	His	Gln	Cys	Ser	Phe	Thr	Thr	Pro		
313						610						615	620					
316	Asp	Val	Asp	Val	Leu	Leu	Phe	His	Tyr	Glu	Ser	Val	His	Glu	Ser	Gln		
317	625						630						635	640				
320	Ala	Ser	Asp	Val	Lys	Gln	Glu	Ala	Asn	His	Leu	Gln	Gly	Ser	Asp	Gly		
321						645						650	655					
324	Gln	Gln	Ser	Val	Lys	Glu	Ser	Lys	Glu	His	Ser	Cys	Thr	Lys	Cys	Asp		
325						660						665	670					
328	Phe	Ile	Thr	Gln	Val	Glu	Glu	Glu	Ile	Ser	Arg	His	Tyr	Arg	Arg	Ala		
329						675						680	685					
332	His	Ser	Cys	Tyr	Lys	Cys	Arg	Gln	Cys	Ser	Phe	Thr	Ala	Ala	Asp	Thr		
333						690						695	700					
336	Gln	Ser	Leu	Leu	Glu	His	Phe	Asn	Thr	Val	His	Cys	Gln	Glu	Gln	Asp		
337	705						710						715	720				
340	Ile	Thr	Thr	Ala	Asn	Gly	Glu	Glu	Asp	Gly	His	Ala	Ile	Ser	Thr	Ile		
341						725						730	735					
344	Lys	Glu	Glu	Pro	Lys	Ile	Asp	Phe	Arg	Val	Tyr	Asn	Leu	Leu	Thr	Pro		
345						740						745	750					
348	Asp	Ser	Lys	Met	Gly	Glu	Pro	Val	Ser	Glu	Ser	Val	Val	Lys	Arg	Glu		
349						755						760	765					
352	Lys	Leu	Glu	Glu	Lys	Asp	Gly	Leu	Lys	Glu	Lys	Val	Trp	Thr	Glu	Ser		
353						770						775	780					
356	Ser	Ser	Asp	Asp	Leu	Arg	Asn	Val	Thr	Trp	Arg	Gly	Ala	Asp	Ile	Leu		
357	785						790						795	800				
360	Arg	Gly	Ser	Pro	Ser	Tyr	Thr	Gln	Ala	Ser	Leu	Gly	Leu	Leu	Thr	Pro		
361						805						810	815					
364	Val	Ser	Gly	Thr	Gln	Glu	Gln	Thr	Lys	Thr	Leu	Arg	Asp	Ser	Pro	Asn		
365						820						825	830					
368	Val	Glu	Ala	Ala	His	Leu	Ala	Arg	Pro	Ile	Tyr	Gly	Leu	Ala	Val	Glu		
369						835						840	845					

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372 Thr Lys Gly Phe Leu Gln Gly Ala Pro Ala Gly Gly Glu Lys Ser Gly
373      850                      855                      860
376 Ala Leu Pro Gln Gln Tyr Pro Ala Ser Gly Glu Asn Lys Ser Lys Asp
377 865                      870                      875                      880
380 Glu Ser Gln Ser Leu Leu Arg Arg Arg Arg Gly Ser Gly Val Phe Cys
381                      885                      890                      895
384 Ala Asn Cys Leu Thr Thr Lys Thr Ser Leu Trp Arg Lys Asn Ala Asn
385                      900                      905                      910
388 Gly Gly Tyr Val Cys Asn Ala Cys Gly Leu Tyr Gln Lys Leu His Ser
389                      915                      920                      925
392 Thr Pro Arg Pro Leu Asn Ile Lys Gln Asn Asn Gly Glu Gln Ile
393      930                      935                      940
396 Ile Arg Arg Arg Thr Arg Lys Arg Leu Asn Pro Glu Ala Leu Gln Ala
397 945                      950                      955                      960
400 Glu Gln Leu Asn Lys Gln Gln Arg Gly Ser Asn Glu Glu Gln Val Asn
401                      965                      970                      975
404 Gly Ser Pro Leu Glu Arg Arg Ser Glu Asp His Leu Thr Glu Ser His
405                      980                      985                      990
408 Gln Arg Glu Ile Pro Leu Pro Ser Leu Ser Lys Tyr Glu Ala Gln Gly
409      995                      1000                      1005
412 Ser Leu Thr Lys Ser His Ser Ala Gln Gln Pro Val Leu Val Ser
413      1010                      1015                      1020
416 Gln Thr Leu Asp Ile His Lys Arg Met Gln Pro Leu His Ile Gln
417      1025                      1030                      1035
420 Ile Lys Ser Pro Gln Glu Ser Thr Gly Asp Pro Gly Asn Ser Ser
421      1040                      1045                      1050
424 Ser Val Ser Glu Gly Lys Gly Ser Ser Glu Arg Gly Ser Pro Ile
425      1055                      1060                      1065
428 Glu Lys Tyr Met Arg Pro Ala Lys His Pro Asn Tyr Ser Pro Pro
429      1070                      1075                      1080
432 Gly Ser Pro Ile Glu Lys Tyr Gln Tyr Pro Leu Phe Gly Leu Pro
433      1085                      1090                      1095
436 Phe Val His Asn Asp Phe Gln Ser Glu Ala Asp Trp Leu Arg Phe
437      1100                      1105                      1110
440 Trp Ser Lys Tyr Lys Leu Ser Val Pro Gly Asn Pro His Tyr Leu
441      1115                      1120                      1125
444 Ser His Val Pro Gly Leu Pro Asn Pro Cys Gln Asn Tyr Val Pro
445      1130                      1135                      1140
448 Tyr Pro Thr Phe Asn Leu Pro Pro His Phe Ser Ala Val Gly Ser
449      1145                      1150                      1155
452 Asp Asn Asp Ile Pro Leu Asp Leu Ala Ile Lys His Ser Arg Pro
453      1160                      1165                      1170
456 Gly Pro Thr Ala Asn Gly Ala Ser Lys Glu Lys Thr Lys Ala Pro
457      1175                      1180                      1185
460 Pro Asn Val Lys Asn Glu Gly Pro Leu Asn Val Val Lys Thr Glu
461      1190                      1195                      1200
464 Lys Val Asp Arg Ser Thr Gln Asp Glu Leu Ser Thr Lys Cys Val
465      1205                      1210                      1215
468 His Cys Gly Ile Val Phe Leu Asp Glu Val Met Tyr Ala Leu His

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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date